

SEQUENCE LISTING

<110> Bates, Elizabeth
Fournier, Nathalie
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Garrone, Pierre

<120> MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND
METHODS

<130> SF0977X

<140> 09/223,919

<141> 1998-12-31

<140> 09/224,604

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tggtctcccc gtcccctgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg 174

Met Gly Arg Pro Leu Leu Leu
-19 -15

ccc cta ctg ccc ctg ctg ctg ccg cca gca ttt ctg cag cct agt ggc 222

Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly
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tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa 270

Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys
5 10 15 20

cac ctc tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc	318
His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe	
25 30 35	
tat tac ccc tgg gag tta gcc aca gct ccc gac gtg aga ata tcc tgg	366
Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp	
40 45 50	
aga cgg ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct	414
Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro	
55 60 65	
tcc att cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag	462
Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu	
70 75 80	
ggt cag aag agc ggc ttc ctc agg atc tcc aac ctg cag aag cag gac	510
Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp	
85 90 95 100	
cag tct gtg tat ttc tgc cga gtt gag ctg gac aca cgg agc tca ggg	558
Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly	
105 110 115	
agg cag cag tgg cag tcc atc gag ggg acc aaa ctc tcc atc acc cag	606
Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln	
120 125 130	
gct gtc acg acc acc acc cag agg ccc agc agc atg act acc acc tgg	654
Ala Val Thr Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Trp	
135 140 145	
agg ctc agt agc aca acc acc aca acc ggc ctc agg gtc aca cag ggc	702
Arg Leu Ser Ser Thr Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly	
150 155 160	
aaa cga cgc tca gac tct tgg cac ata agt ctg gag act gct gtg ggg	750
Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly	
165 170 175 180	
gtg gca gtg gct gtc act gtg ctc gga atc atg att ttg gga ctg atc	798
Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile	
185 190 195	
tgc ctc ctc agg tgg agg aga agg aaa ggt cag cag cgg act aaa gcc	846
Cys Leu Leu Arg Trp Arg Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala	
200 205 210	
aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag	894
Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu	
215 220 225	
aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag	942
Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys	
230 235 240	

gat gac ggc atc gta tat gct tcc ctt gcc ctc tcc agc tcc acc tca 990
 Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser
 245 250 255 260

ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag 1038
 Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
 265 270 275

acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa 1092
 Thr Leu Tyr Ser Val Leu Lys Ala
 280

tgggtgaggcc aggtacagtg gcgcacacct gtaatcccag ctactctgaa gcctgaggca 1152
 gaatcaagtg agcccaggag ttcagggcca gctttgataa tggagcgaga tgccatctct 1212
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 Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
 15 20 25
 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
 30 35 40 45
 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
 50 55 60
 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 65 70 75
 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
 80 85 90
 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
 95 100 105
 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
 110 115 120 125
 Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro
 130 135 140
 Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr
 145 150 155

Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
 160 165 170
 Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
 175 180 185
 Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
 190 195 200 205
 Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
 210 215 220
 Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
 225 230 235
 Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
 240 245 250
 Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
 255 260 265
 Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
 270 275 280

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 ctccacaggg cccctctcct gcttggacgg ctctgctggt ctcccgtcc cctggagaag 120
 aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg 168
 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu
 -17 -15 -10 -5
 ctg ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca 216
 Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro
 1 5 10
 agc tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg 264
 Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met
 15 20 25

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gcc aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac Ala Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His 45 50 55 60	360
ggg cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr 65 70 75	408
gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe 80 85 90	456
ctc agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys 95 100 105	504
cga gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc Arg Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser 110 115 120	552
atc gag ggg acc aaa ctc tcc atc acc cag ggt cag cag cgg act aaa Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys 125 130 135 140	600
gcc aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr 145 150 155	648
gag aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro 160 165 170	696
aag gat gac ggc atc gtc tat gct tcc ctt gcc ctc tcc agc tcc acc Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr 175 180 185	744
tca ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac Ser Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn 190 195 200	792
gag acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct Glu Thr Leu Tyr Ser Val Leu Lys Ala 205 210	839
caagactgaa tgggtgaggcc aggtacagtg gcgcacacct gtaatcccag ctactctgaa	899
gcctgaggca gaatcaagtg agcccaggag ttcagggcca gctt	943
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cagacatctg tgcctcatte ctgatctcaa ggggaaagca agaacaaggg aggccttcctc	180
aggatctcga acctgcggaa ggaggaccag tctgtgtact tctgccaaagt ccagctggac	240
atacagatca gggaggctgt cgtggcagtc catcaagggg acccacctca ccatcaccca	300
ggccctcagg cagccctccc acagggcccc tctcctgcct ggacagctct gctggctctcc	360
ccgtcccttg gagaagaaca aggcc atg ggt cgg ccc ctg ctg ctg ccc ctg	412
Met Gly Arg Pro Leu Leu Leu Pro Leu	
-17 -15 -10	
ctg ctc ctg ctg cag ccg cca gca ttt ctg cag cct ggt ggc tcc aca	460
Leu Leu Leu Leu Gln Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr	
-5 1 5	
gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa cac ctc	508
Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu	
10 15 20	
tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc tat tac	556
Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr	
25 30 35 40	
ccc tgg gag tta gcc ata gtt ccc aac gtg aga ata tcc tgg aga cgg	604
Pro Trp Glu Leu Ala Ile Val Pro Asn Val Arg Ile Ser Trp Arg Arg	
45 50 55	
ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct tcc att	652
Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile	
60 65 70	
cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag	700
His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln	
75 80 85	
gag agc ggc ttc ctc agg atc tca aac ctg cgg aag gag gac cag tct	748
Glu Ser Gly Phe Leu Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser	
90 95 100	
gtg tat ttc tgc cga gtc gag ctg gac acc cgg aga tca ggg agg cag	796
Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln	
105 110 115 120	
cag ttg cag tcc atc aag ggg acc aaa ctc acc atc acc cag gct gtc	844
Gln Leu Gln Ser Ile Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val	
125 130 135	
aca acc acc acc acc tgg agg ccc agc agc aca acc acc ata gcc ggc	892
Thr Thr Thr Thr Thr Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly	
140 145 150	
ctc agg gtc aca gaa agc aaa ggg cac tca gaa tca tgg cac cta agt	940
Leu Arg Val Thr Glu Ser Lys Gly His Ser Glu Ser Trp His Leu Ser	
155 160 165	
ctg gac act gcc atc agg gtt gca ttg gct gtc gct gtg ctc aaa act	988
Leu Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr	
170 175 180	

gtc att ttg gga ctg ctg tgc ctc ctc ctc ctg tgg tgg agg aga agg 1036
 Val Ile Leu Gly Leu Leu Cys Leu Leu Leu Trp Trp Arg Arg Arg
 185 190 195 200

aaa ggt agc agg gcg cca agc agt gac ttc tgaccaacag agtgtgggga 1086
 Lys Gly Ser Arg Ala Pro Ser Ser Asp Phe
 205 210

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 aaaa 1450

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Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
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Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Ile Val
 35 40 45

Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
 50 55 60

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 65 70 75

Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
 80 85 90 95

Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
 100 105 110

Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
 115 120 125

Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr Trp Arg
 130 135 140

Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
 145 150 155

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
 160 165 170 175
 Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
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 Ser Asp Phe
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 aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg ctg 171
 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu
 -15 -10 -5
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 Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser
 -1 1 5 10
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 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
 15 20 25
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 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45
 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 363
 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60
 cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 411
 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75
 aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc ctc 459
 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
 80 85 90

agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc cga 507
 Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc atc 555
 Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
 110 115 120 125

gag ggg acc aaa ctc tcc atc acc cag ggg aac cct tcc aaa aca cag 603
 Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Asn Pro Ser Lys Thr Gln
 130 135 140

agg agc cat atg aga ata tca gga atg aag gac aaa ata cag atc cca 651
 Arg Ser His Met Arg Ile Ser Gly Met Lys Asp Lys Ile Gln Ile Pro
 145 150 155

agc taa atcccaagga tgacggcatc gtctatgctt cccttgccct ctccagctcc 707
 Ser

acctcaccca gagcacctcc cagccaccgt cccctcaaga gccccagaa cgagaccctg 767

tactctgtct taaaggccta accaatggac agccctctca agactgaatg gtgaggccag 827

gtacagtggc gcacacctgt aatcccagct actctgaagc ctgaggcaga atcaagtga 887

cccaggagtt cagggccagc tt 909

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Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
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Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45

Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60

Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75

Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
 80 85 90

Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
 110 115 120 125

Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Asn Pro Ser Lys Thr Gln
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Arg Ser His Met Arg Ile Ser Gly Met Lys Asp Lys Ile Gln Ile Pro
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 ataaaggaag tgctggtcac cctggaggtg tactggtttg gggaagggtcc ccggccccc 180
 cagccctctg gggagcctca ccctggctct cccactcac ctgagccctc aggcagcccc 240
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 Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser
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 tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg ggt 446
 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
 15 20 25
 ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 494
 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45
 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 542
 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60
 cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 590
 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75
 aac cgg ctc ttt ctg aac tgg aca gag ggt cag gag agc ggc ttc ctc 638
 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu
 80 85 90

agg atc tca aac ctg cgg aag gag gac cag tct gtg tat ttc tgc cga 686
 Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

gtc gag ctg gac acc cgg aga tca ggg agg cag cag ttg cag tcc atc 734
 Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile
 110 115 120 125

aag ggg acc aaa ctc acc atc acc cag gct gtc aca acc acc acc acc 782
 Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr
 130 135 140

tgg agg ccc agc agc aca acc acc ata gcc ggc ctc agg gtc aca gaa 830
 Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu
 145 150 155

agc aaa ggg cac tca gaa tca tgg cac cta agt ctg gac act gcc atc 878
 Ser Lys Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile
 160 165 170

agg gtt gca ttg gct gtc gct gtg ctc aaa act gtc att ttg gga ctg 926
 Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu
 175 180 185

ctg tgc ctc ctc ctg tgg tgg agg aga agg aaa ggt agc agg gcg cca 974
 Leu Cys Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro
 190 195 200 205

agc agt gac ttc tga ccaacagagt gtggggagaa gggatgtgta ttagccccgg 1029
 Ser Ser Asp Phe

aggacgtgat gtgagacccg cttgtgagtc ctccacactc gttccccatt ggcaagatac 1089

atggagagca ccctgaggac ctttaaaagg caaagccgca aggcagaagg aggctggggtc 1149

cctgaatcac cgactggagg agagttacct acaagagcct tcatccagga gcatccacac 1209

tgcaatgata taggaatgag gtctgaactc cactgaatta aaccactggc atttgggggc 1269

tgttcattat agcagtgcaa agagtccctt tatcctcccc aaggatggaa aatacaattt 1329

attttgctta ccatacaccc cttttctcct cgtccacatt ttccaatctg tatggtggct 1389

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Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
 15 20 25

Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45
 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60
 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75
 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu
 80 85 90
 Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg
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